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## Jacobian



Given a set  $\mathbf{y} = \mathbf{f}(\mathbf{x})$  of n equations in n variables  $x_1, ..., x_n$ , written explicitly as

$$\mathbf{y} \equiv \begin{bmatrix} f_1(\mathbf{x}) \\ f_2(\mathbf{x}) \\ \vdots \\ f_n(\mathbf{x}) \end{bmatrix}, \tag{1}$$

or more explicitly as

$$\begin{cases} y_1 = f_1(x_1, \dots, x_n) \\ \vdots \\ y_n = f_n(x_1, \dots, x_n), \end{cases}$$
 (2)

the Jacobian matrix, sometimes simply called "the Jacobian" (Simon and Blume 1994) is defined by

$$J(x_1, \dots, x_n) = \begin{bmatrix} \frac{\partial y_1}{\partial x_1} & \dots & \frac{\partial y_1}{\partial x_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial y_n}{\partial x_1} & \dots & \frac{\partial y_n}{\partial x_n} \end{bmatrix}.$$
 (3)

The determinant of  $\, J \,$  is the Jacobian determinant (confusingly, often called "the Jacobian" as well) and is denoted

$$J = \left| \frac{\partial(y_1, \dots, y_n)}{\partial(x_1, \dots, x_n)} \right|. \tag{4}$$

The Jacobian matrix and determinant can be computed using the Mathematica commands

Taking the differential

$$d\mathbf{v} = \mathbf{v}_{\mathbf{x}} d\mathbf{x} \tag{5}$$

shows that J is the determinant of the matrix  $y_x$ , and therefore gives the ratios of n-dimensional volumes (contents) in y and x,

$$du_1 \cdots du_n = \left| \frac{\partial (y_1, \dots, y_n)}{\partial x_1} \right| dx_1 \cdots dx_n$$
 (6)

14942, ... , 491 / 3

It therefore appears, for example, in the change of variables theorem.

The concept of the Jacobian can also be applied to n functions in more than n variables. For example, considering f(u,v,w) and g(u,v,w), the Jacobians

$$\frac{\partial(f,g)}{\partial(u,v)} \qquad = \qquad \begin{vmatrix} f_u & f_v \\ g_u & g_v \end{vmatrix} \tag{7}$$

$$\frac{\partial(f,g)}{\partial(u,w)} \qquad = \qquad \begin{vmatrix} f_u & f_w \\ g_u & g_w \end{vmatrix} \tag{8}$$

can be defined (Kaplan 1984, p. 99).

For the case of n = 3 variables, the Jacobian takes the special form

$$Jf(x_1, x_2, x_3) \equiv \left| \frac{\partial \mathbf{y}}{\partial x_1} \cdot \frac{\partial \mathbf{y}}{\partial x_2} \times \frac{\partial \mathbf{y}}{\partial x_3} \right|, \tag{9}$$

where  $a \cdot b$  is the dot product and  $b \times c$  is the cross product, which can be expanded to give

$$\left| \begin{array}{c} \frac{\partial (y_1, y_2, y_3)}{\partial (x_1, x_2, x_2)} \right| = \left| \begin{array}{ccc} \frac{\partial y_1}{\partial x_1} & \frac{\partial y_1}{\partial x_2} & \frac{\partial y_1}{\partial x_3} \\ \frac{\partial y_2}{\partial x_1} & \frac{\partial y_2}{\partial x_2} & \frac{\partial y_2}{\partial x_3} \\ \frac{\partial y_3}{\partial x_1} & \frac{\partial y_3}{\partial x_2} & \frac{\partial y_3}{\partial x_3} \end{array} \right|. \tag{10}$$

SEE ALSO: Change of Variables Theorem, Curvilinear Coordinates, Hessian, Implicit Function Theorem, Multivariable Calculus, Wronskian

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Classic techniques for simulating molecular motion, such as the Monte Carlo and molecular dynamics methods, generate individual motion pathways one at a time and spend most of their time trying to escape from the local minima of the energy landscape of a molecule. Their high computational cost prevents them from being used to analyze many pathways. We introduce Stochustic Roadmap Sirrrcllation (SRS), a new approach for exploring the kinetics of molecular motion by simultaneously examining multip ...

3 ProtoMol, an object-oriented framework for prototyping novel algorithms for molecular dynamics



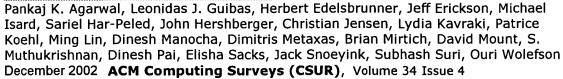
Thierry Matthey, Trevor Cickovski, Scott Hampton, Alice Ko, Qun Ma, Matthew Nyerges, Troy Raeder, Thomas Slabach, Jesús A. Izaguirre
September 2004 ACM Transactions on Mathematical Software (TOMS), Volume 30 Issue 3

Full text available: pdf(911.92 KB) Additional Information: full citation, abstract, references, index terms

ProtoMol is a high-performance framework in C++ for rapid prototyping of novel algorithms for molecular dynamics and related applications. Its flexibility is achieved primarily through the use of inheritance and design patterns (object-oriented programming). Performance is obtained by using templates that enable generation of efficient code for sections critical to performance (generic programming). The framework encapsulates important optimizations that can be used by developers, such as parall ...

**Keywords**: Fast electrostatic methods, incremental parallelism, molecular dynamics, multigrid, multiple time-stepping integration, object-oriented framework.

## 4 Algorithmic issues in modeling motion



Full text available: pdf(205.25 KB) Additional Information: full citation, abstract, references, citings, index terms

This article is a survey of research areas in which motion plays a pivotal role. The aim of the article is to review current approaches to modeling motion together with related data structures and algorithms, and to summarize the challenges that lie ahead in producing a more unified theory of motion representation that would be useful across several disciplines.

**Keywords**: Computational geometry, computer vision, mobile networks, modeling, molecular biology, motion modeling, physical simulation, robotoics, spatio-temporal databases

## Demonstrating the scalability of a molecular dynamics application on a Petaflop computer

George S. Almasi, Călin Caşcaval, José G. Castaños, Monty Denneau, Wilm Donath, Maria Eleftheriou, Mark Giampapa, Howard Ho, Derek Lieber, José E. Moreira, Dennis Newns, Marc Snir, Henry S. Warren

June 2001 Proceedings of the 15th international conference on Supercomputing

Full text available: pdf(392.72 KB) Additional Information: full citation, abstract, references, citings, index terms

The IBM Blue Gene project has endeavored into the development of a cellular architecture computer with millions of concurrent threads of execution. One of the major challenges of this project is demonstrating that applications can successfully exploit this massive amount of parallelism. Starting from the sequential version of a well known molecular dynamics code, we developed a new application that exploits the multiple levels of parallelism in the Blue Gene cellular architecture. We perform ...

**Keywords**: Blue Gene, cellular architecture, massively parallel computing, molecular dynamics, performance evaluation



Visualization: Visualization of molecular quantum dynamics: a molecular visualization tool with integrated Web3D and haptics
 R. Andrew Davies, Nigel W. John, John N. MacDonald, Keith H. Hughes



R. Andrew Davies, Nigel W. John, John N. MacDonald, Keith H. Hughes
March 2005 Proceedings of the tenth international conference on 3D Web
technology

Full text available: pdf(1.78 MB) Additional Information: full citation, abstract, references, index terms

The Department of Chemistry and the School of Informatics at the University of Wales, Bangor are working together to create tools for the visualization of molecular quantum dynamics. This paper presents the results of our initial work. A prototype Molecular Visualiser (MV) application has been developed based on Web3D standards, plus extensions for support of haptic interaction. MV provides the user with visualizations of molecular systems, potential energy surfaces, and wavepacket dynamics. The ...

Keywords: VRML, haptics, molecular quantum dynamics, visualization

Molecular simulation of rheological properties using massively parallel supercomputers



R. K. Bhupathiraju, S. T. Cui, S. Gupta, H. D. Cochran, P. T. Cummings November 1996 **Proceedings of the 1996 ACM/IEEE conference on Supercomputing (CDROM) - Volume 00** 

Full text available: pdf(120.44 KB) Additional Information: full citation, abstract, references, index terms

Advances in parallel supercomputing now make possible molecular-based engineering and science calculations that will soon revolutionize many technologies, such as those involving polymers and those involving aqueous electrolytes. We have developed a suite of message-passing codes for classical molecular simulation of such complex fluids and amorphous materials and have completed a number of demonstration calculations of problems of scientific and technological importance with each (describe ...

**Keywords**: Molecular dynamics, domain decomposition, molecular simulation, nonequilibrium, rheology

Simulating the dynamics of auroral phenomena
 Gladimir V. G. Baranoski, Justin Wan, Jon G. Rokne, Ian Bell
 January 2005 ACM Transactions on Graphics (TOG), Volume 24 Issue 1



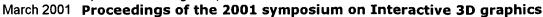
Full text available: pdf(214.56 KB) Additional Information: full citation, abstract, references, index terms

Simulating natural phenomena has always been a focal point for computer graphics research. Its importance goes beyond the production of appealing presentations, since research in this area can contribute to the scientific understanding of complex natural processes. The natural phenomena, known as the Aurora Borealis and Aurora Australis, are geomagnetic phenomena of impressive visual characteristics and remarkable scientific interest. Aurorae present a complex behavior that arises from intera ...

**Keywords**: Atmospheric effects, natural phenomena, plasma phenomena, rendering

## A system for interactive molecular dynamics simulation

John E. Stone, Justin Gullingsrud, Klaus Schulten



Full text available: 📆 pdf(129.46 KB) Additional Information: full citation, references, citings, index terms

Keywords: haptic feedback, molecular dynamics, steered molecular dynamics

10 Session P8: nature visualization: Visualizing dynamic molecular conformations Johannes Schmidt-Ehrenberg, Daniel Baum, Hans Christian Hege

October 2002 Proceedings of the conference on Visualization '02

Full text available: pdf(2.72 MB) Additional Information: full citation, abstract, references, index terms

The bioactivity of a molecule strongly depends on its metastable conformational shapes and the transitions between these. Therefore, conformation analysis and visualization is a basic prerequisite for the understanding of biochemical processes. We present techniques for visual analysis of metastable molecular conformations. Core of these are flexibly applicable methods for alignment of molecular geometries, as well as methods for depicting shape and 'fuzziness' of metastable conformations. All an ...

**Keywords**: drug design, molecular conformation analysis, molecular modeling, uncertainty visualization

### 11 A modeling system based on dynamic constraints

Ronen Barzel, Alan H. Barr

June 1988 ACM SIGGRAPH Computer Graphics, Proceedings of the 15th annual conference on Computer graphics and interactive techniques, Volume 22 Issue 4

Additional Information: full citation, abstract, references, citings, index Full text available: pdf(4.29 MB) terms

We present "dynamic constraints," a physically-based technique for constraint-based control of computer graphics models. Using dynamic constraints, we build objects by specifying geometric constraints; the models assemble themselves as the elements move to satisfy the constraints. The individual elements are rigid bodies which act in accordance with the rules of physics, and can thus exhibit physically realistic behavior. To implement the constraints, a set of "constraint forces" is found, which ...

Keywords: contraints, dynamics, modeling, simulation

## 12 Animation of dynamic legged locomotion

Marc H. Raibert, Jessica K. Hodgins

July 1991 ACM SIGGRAPH Computer Graphics, Proceedings of the 18th annual conference on Computer graphics and interactive techniques, Volume 25 Issue 4

Additional Information: full citation, abstract, references, citings, index Full text available: pdf(1.72 MB) terms

This paper is about the use of control algorithms to animate dynamic legged locomotion. Control could free the animator from specifying the details of joint and limb motion while producing both physically realistic and natural looking results. We implemented computer animations of a biped robot, a quadruped robot, and a kangaroo. Each creature was modeled as a linked set of rigid bodies with compliant





actuators at its joints. Control algorithms regulated the running speed, organized use of the I ...

**Keywords**: computer animation, dynamical simulation, legged locomotion, motion control, physically realistic modeling, robotics

### 13 VRML molecular dynamics trajectories

Geoff Leach, James Gilbert

February 1999 Proceedings of the fourth symposium on Virtual reality modeling language

Full text available: pdf(2.25 MB) Additional Information: full citation, references, index terms

Keywords: VRML, compression, molecular dynamics, scientific visualisation

## 14 Scalable molecular dynamics for large biomolecular systems

Robert K. Brunner, James C. Phillips, Laxmikant V. Kale

November 2000 Proceedings of the 2000 ACM/IEEE conference on Supercomputing (CDROM)

Full text available: pdf(211.89 KB) Additional Information: full citation, abstract, references, citings, index terms

We present an optimized parallelization scheme for molecular dynamics simulations of large biomolecular systems, implemented in the production-quality molecular dynamics program NAMD. With an object-based hybrid force and spatial decomposition scheme, and an aggressive measurement-based predictive load-balancing framework, we have attained speeds and speedups that are much higher than any reported in literature so far. The paper first summarizes the broad methodology we are pu ...

# 15 Computational fluid dynamics in a traditional animation environment Patrick Witting

July 1999 Proceedings of the 26th annual conference on Computer graphics and interactive techniques

Full text available: pdf(734.22 KB) Additional Information: full citation, references, citings, index terms

**Keywords:** animation, animation systems, applications, fluid simulations, natural phenomena, numerical analysis, physically based animation, physically based modeling, scientific visualization, texture mapping

#### 16 Modeling the motion of a hot, turbulent gas

Nick Foster, Dimitris Metaxas

August 1997 Proceedings of the 24th annual conference on Computer graphics and interactive techniques

Full text available: pdf(5.92 MB) Additional Information: full citation, references, citings

**Keywords:** animation, convection, gas simulations, gaseous phenomena, physics-based modeling, smoke, steam, turbulent flow



# 17 Simulation, motion capture, editing: Modeling tension and relaxation for computer animation



Michael Neff, Eugene Fiume

# July 2002 Proceedings of the 2002 ACM SIGGRAPH/Eurographics symposium on Computer animation

Full text available: pdf(3.44 MB)

Additional Information: <u>full citation</u>, <u>abstract</u>, <u>references</u>, <u>citings</u>, <u>index</u> terms

The use of tension and relaxation in the muscles of real creatures gives rise to nuanced motion that conveys emotion or intent. Artists have long exploited knowledge of this in traditional animation and other areas, but it has been both overlooked and difficult to achieve in physically based animation. The robotically stiff motion that has come to typify physically based approaches belies the fact that dynamics has much to offer in facilitating far more subtle motion in which animators could fre ...

**Keywords**: animation, human body simulation, physically based animation

18 Parallel approaches to short range molecular dynamics simulations

Pablo Tamayo, Jill P. Mesirov, Bruce M. Boghosian

August 1991 Proceedings of the 1991 ACM/IEEE conference on Supercomputing

Full text available: pdf(818.30 KB) Additional Information: full citation, references, citings, index terms

19 Simulation and preferences: Virtual spring manipulators for particle steering in molecular dynamics on the responsive workbench



Michal Koutek, Jeroen van Hees, Frits H. Post, A. F. Bakker

May 2002 Proceedings of the workshop on Virtual environments 2002

Full text available: pdf(6.52 MB) Additional Information: full citation, abstract, references, citings

In this paper we present new virtual spring manipulator-based tools for steering particles in molecular dynamics simulations in virtual environments. We briefly overview the MolDRIVE system, our visualization and computational steering environment for molecular dynamics real-time simulations, which is the platform for our particle steering implementation. Our study concentrates on visual feedback tools. We compare a basic virtual particle steering method with two other methods using a spring mani ...

20 An 8.61 Tflop/s molecular dynamics simulation for NaCl with a special-purpose



computer: MDM

Tetsu Narumi, Atsushi Kawai, Takahiro Koishi

November 2001 Proceedings of the 2001 ACM/IEEE conference on Supercomputing (CDROM)

Full text available: pdf(1.19 MB) Additional Information: full citation, abstract, references, index terms

We performed molecular dynamics (MD) simulation of 33 million pairs of NaCl ions with the Ewald summation and obtained a calculation speed of 8.61 Tflop/s. In this calculation we used a special-purpose computer, MDM, which we have developed for the calculations of the Coulomb and van der Waals forces. The MDM enabled us to perform large scale MD simulations without truncating the Coulomb force. It is composed of MDGRAPE-2, WINE-2 and a host computer. MDGRAPE-2 accelerates the calculation for rea ...

**Keywords:** ewald method, molecular dynamics simulation, special-purpose computer

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81 An analytic approach to significance assessment in local sequence alignment with gaps

R. Bundschuh

April 2000 Proceedings of the fourth annual international conference on Computational molecular biology

Full text available: pdf(974.15 Additional Information: full citation, abstract, references, citings

A detailed study of the Smith-Waterman alignment algorithm is performed in order to find an analytical approach to the problem of assessing the statistical significance of local alignments with gaps. The significance is shown to be given in terms of an eigenvalue equation which captures the dynamics of the much simpler global alignment algorithm. This eigenvalue equation is then explicitly solved for a simple scoring system and the resulting significance estimations are verified by a comparis ...

Keywords: Gumbel distribution, sequence alignment, statistical significance

82 Protein structure determination using protein threading and sparse NMR data (extended abstract)

Ying Xu, Dong Xu, Oakley H. Crawford, J. Ralph Einstein, Engin Serpersu April 2000 Proceedings of the fourth annual international conference on

Computational molecular biology Full text available: pdf(663.42 Additional Information: full citation, abstract, references, citings

It is well known that the NMR method for protein structure determination applies to small proteins and that its effectiveness decreases very rapidly as the molecular weight increases beyond about 30 kD. We have recently developed a method for protein structure determination that can fully utilize partial NMR data as calculation constraints. The core of the method is a threading algorithm that quarantees to find a globally optimal alignment between a query sequence and a template structure, ...

Keywords: NMR, energy minimization, fold recognition, protein structure

determination, protein threading

### 83 HPFBench: a high performance Fortran benchmark suite



Y. Charlie Hu, Guohua Jin, S. Lennart Johnsson, Dimitris Kehagias, Nadia Shalaby March 2000 **ACM Transactions on Mathematical Software (TOMS)**, Volume 26 Issue 1

Full text available: pdf(274.52 KB)

Additional Information: <u>full citation</u>, <u>abstract</u>, <u>references</u>, <u>citings</u>, index terms

The high performance Fortran (HPF) benchmark suite HPFBench is designed for evaluating the HPF language and compilers on scalable architectures. The functionality of the benchmarks covers scientific software library functions and application kernels that reflect the computational structure and communication patterns in fluid dynamic simulations, fundamental physics, and molecular studies in chemistry and biology. The benchmarks are characterized in terms of FLOP count, memory usage, communi ...

**Keywords**: benchmarks, compilers, high performance Fortran

## 84 Pattern matching in dynamic texts



Stephen Alstrup, Gerth Stølting Brodal, Theis Rauhe

February 2000 Proceedings of the eleventh annual ACM-SIAM symposium on Discrete algorithms

Full text available: pdf(985.73 KB)

Additional Information: <u>full citation</u>, <u>references</u>, <u>citings</u>, <u>index terms</u>

### 85 Algorithmic strategies in combinatorial chemistry



Deborah Goldman, Sorin Istrail, Giuseppe Lancia, Antonio Piccolboni, Brian Walenz February 2000 Proceedings of the eleventh annual ACM-SIAM symposium on Discrete algorithms

Full text available: pdf(940.84 KB)

Additional Information: full citation, references, index terms

# 86 Computational fluid dynamics in a traditional animation environment



Patrick Witting

July 1999 Proceedings of the 26th annual conference on Computer graphics and interactive techniques

Full text available: pdf(734.22 KB)

Additional Information: full citation, references, citings, index terms

**Keywords**: animation, animation systems, applications, fluid simulations, natural phenomena, numerical analysis, physically based animation, physically based modeling, scientific visualization, texture mapping

## 87 Distance browsing in spatial databases



Gísli R. Hjaltason, Hanan Samet

June 1999 ACM Transactions on Database Systems (TODS), Volume 24 Issue 2

Full text available: pdf(460.81 KB)

Additional Information: full citation, abstract, references, citings, index terms

We compare two different techniques for browsing through a collection of spatial objects stored in an R-tree spatial data structure on the basis of their distances from an arbitrary spatial query object. The conventional approach is one that makes use of a k-nearest neighbor algorithm where k is known prior to the invocation of the algorithm. Thus if m < k neighbors are needed, the k-nearest neighbor alg ...

**Keywords**: R-trees, distance browsing, hiearchical spatial data structures. nearest neighbors, ranking

88 Complexity theory column 24: Biomolecular computing: recent theoretical and experimental advances



Lane A. Hemaspaandra

June 1999 ACM SIGACT News, Volume 30 Issue 2

Full text available: pdf(573.28

Additional Information: full citation, abstract, references

And so summer comes around again. What a good time to relax on the beach (with your theorem notebook), to go on that long-planned family vacation (certainly with your theorem notebook, and don't forget to bring the family) and, above all, to catch up on all the papers and progress that have been piling up during the academic year on your "if only I had the time" list. The current column may save you some time on this! In 1997, Mitsunori Ogihara and Animesh Ray, jointly with Kimberly Smith, wrote ...

89 Improving cache performance in dynamic applications through data and computation reorganization at run time



Chen Ding, Ken Kennedy

May 1999 ACM SIGPLAN Notices, Proceedings of the ACM SIGPLAN 1999 conference on Programming language design and implementation, Volume 34 Issue 5

Full text available: pdf(1.54 MB) Additional Information: full citation, abstract, references, citings, index terms

With the rapid improvement of processor speed, performance of the memory hierarchy has become the principal bottleneck for most applications. A number of compiler transformations have been developed to improve data reuse in cache and registers, thus reducing the total number of direct memory accesses in a program. Until now, however, most data reuse transformations have been static---applied only at compile time. As a result, these transformations cannot be used to optimize irregular and ...

90 Searching gene transfers on Bacillus subtilis using hidden Markov models Laurent Bize, Florence Muri, Franck Samson, François Rodolphe, S. Dusko Ehrlich, Bernard Prum, Philippe Bessières



April 1999 Proceedings of the third annual international conference on Computational molecular biology

Full text available: pdf(738.72 KB)

Additional Information: full citation, references, index terms

91 Large scale molecular dynamics simulations with fast multipole implementations



Zhiqiang Wang, James A. Lupo, Alan M. McKenney, Ruth Pachter January 1999 Proceedings of the 1999 ACM/IEEE conference on Supercomputing (CDROM)

Full text available: pdf(748.81 KB)

Additional Information: <u>full citation</u>, <u>references</u>, <u>citings</u>, <u>index terms</u>

## 92 A unifying data structure for hierarchical methods

Faith E. Sevilgen, Srinivas Aluru

January 1999 Proceedings of the 1999 ACM/IEEE conference on Supercomputing (CDROM)

Full text available: pdf(88.91 KB) Additional Information: full citation, references, index terms

## 93 Parallel implementation of a molecular dynamics simulation program

Alan Mink, Christophe Bailly

December 1998 Proceedings of the 30th conference on Winter simulation

Full text available: pdf(100.62 KB)

Additional Information: full citation, references, index terms

#### 94 Recipes for adjoint code construction

Ralf Giering, Thomas Kaminski

December 1998 ACM Transactions on Mathematical Software (TOMS), Volume 24 Issue 4

Full text available: pdf(301.79 KB)

Additional Information: <u>full citation</u>, <u>abstract</u>, <u>references</u>, <u>citings</u>, index terms

Adjoint models are increasingly being developed for use in meteorology and oceanography. Typical applications are data assimilation, model tuning, sensitivity analysis, and determination of singular vectors. The adjoint model computes the gradient of a cost function with respect to control variables. Generation of adjoint code may be seen as the special case of differentiation of algorithms in reverse mode, where the dependent function is a scalar. The described method for adjoint code gene ...

**Keywords**: adjoint model, adjoint operator, automatic differentiation, computational differentiation, data assimilation, differentiation of algorithms, implicit functions, inverse modeling, optimization, reverse mode

## 95 A parallel rendezvous algorithm for interpolation between multiple grids

Steve Plimpton, Bruce Hendrickson, James Stewart

November 1998 Proceedings of the 1998 ACM/IEEE conference on Supercomputing (CDROM)

Full text available: html(37.23 KB)

 $\mbox{Additional Information:} \ \underline{\mbox{full citation, abstract, references}}, \ \underline{\mbox{citings}}$ 

A number of computational procedures employ multiple grids on which solutions are computed. For example, in multi-physics simulations a primary grid may be used to compute mechanical deformation of an object while a secondary grid is used for thermal conduction calculations. When modeling coupled thermo-mechanical effects, solution data must be interpolated back and forth between the grids each timestep. On a parallel machine, this grid transfer operation can be challenging if the two grids are ...

**Keywords:** grid transfer, load-balancing, multi-physics, multigrid, parallel computing

# 96 A hierarchical load-balancing framework for dynamic multithreaded computations



Vijay Karamcheti, Andrew A. Chien

November 1998 Proceedings of the 1998 ACM/IEEE conference on Supercomputing (CDROM)

Full text available: pdf(120.01 KB)

Additional Information: <u>full citation</u>, <u>abstract</u>, <u>references</u>

High-level parallel programming models that support dynamic fine-grained threads in a global object space, are becoming increasingly popular for expressing irregular applications based on sophisticated adaptive algorithms and pointer-based data structures. However, implementing these multithreaded computations on scalable parallel machines poses significant challenges, particularly with respect to load-balancing. Load-balancing techniques must simultaneously incur low overhead to support fine-gr ...

# 97 Application level scheduling of gene sequence comparison on metacomputers



Neil Spring, Rich Wolski

July 1998 Proceedings of the 12th international conference on Supercomputing

Full text available: pdf(1.35 MB) Additional Information: full citation, references, citings, index terms

## 98 On approximating arbitrary metrices by tree metrics



Yair Bartal

May 1998 Proceedings of the thirtieth annual ACM symposium on Theory of computing

Full text available: pdf(4.11 MB) Additional Information: full citation, references, citings, index terms

## 99 Using prediction to accelerate coherence protocols



Shubhendu S. Mukherjee, Mark D. Hill

April 1998 ACM SIGARCH Computer Architecture News, Proceedings of the 25th annual international symposium on Computer architecture, Volume 26 Issue 3

Full text available: pdf(1.71 MB) Additional Information: full citation, abstract, references, citings, index terms

Most large shared-memory multiprocessors use directory protocols to keep per-processor caches coherent. Some memory references in such systems, however, suffer long latencies for misses to remotely-cached blocks. To ameliorate this latency, researchers have augmented standard coherence protocols with optimizations for specific sharing patterns, such as read-modify-write, producer-consumer, and migratory sharing. This paper seeks to replace these directed solutions with general prediction logic t ...

## 100 An algorithm for finding novel gapped motifs in DNA sequences

Emily Rocke, Martin Tompa

March 1998 Proceedings of the second annual international conference on Computational molecular biology

Full text available: pdf(643.93 KB)

Additional Information: full citation, references, citings, index terms

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